Efficient Correction for EM Connectomics with Skeletal Representation

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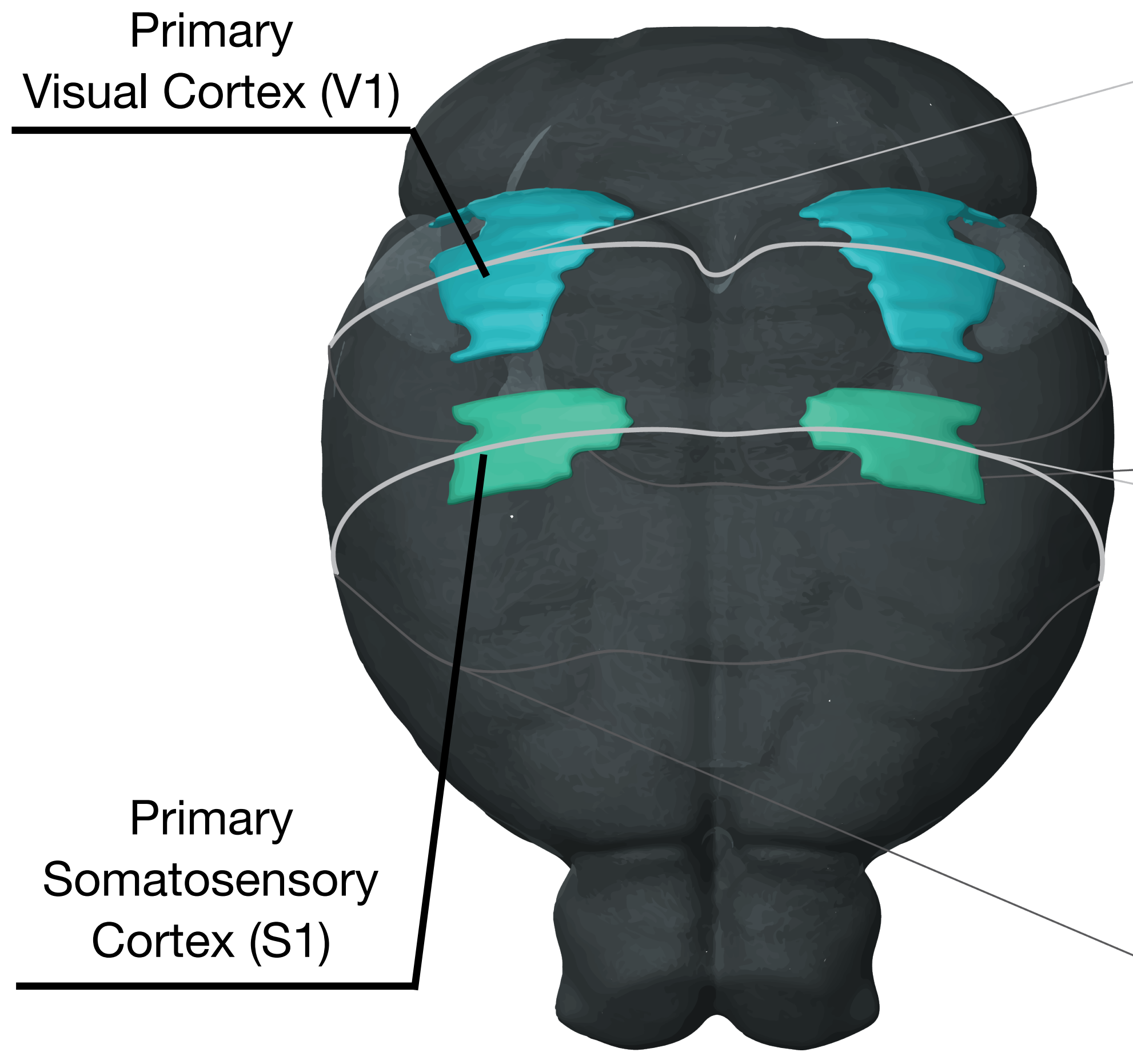
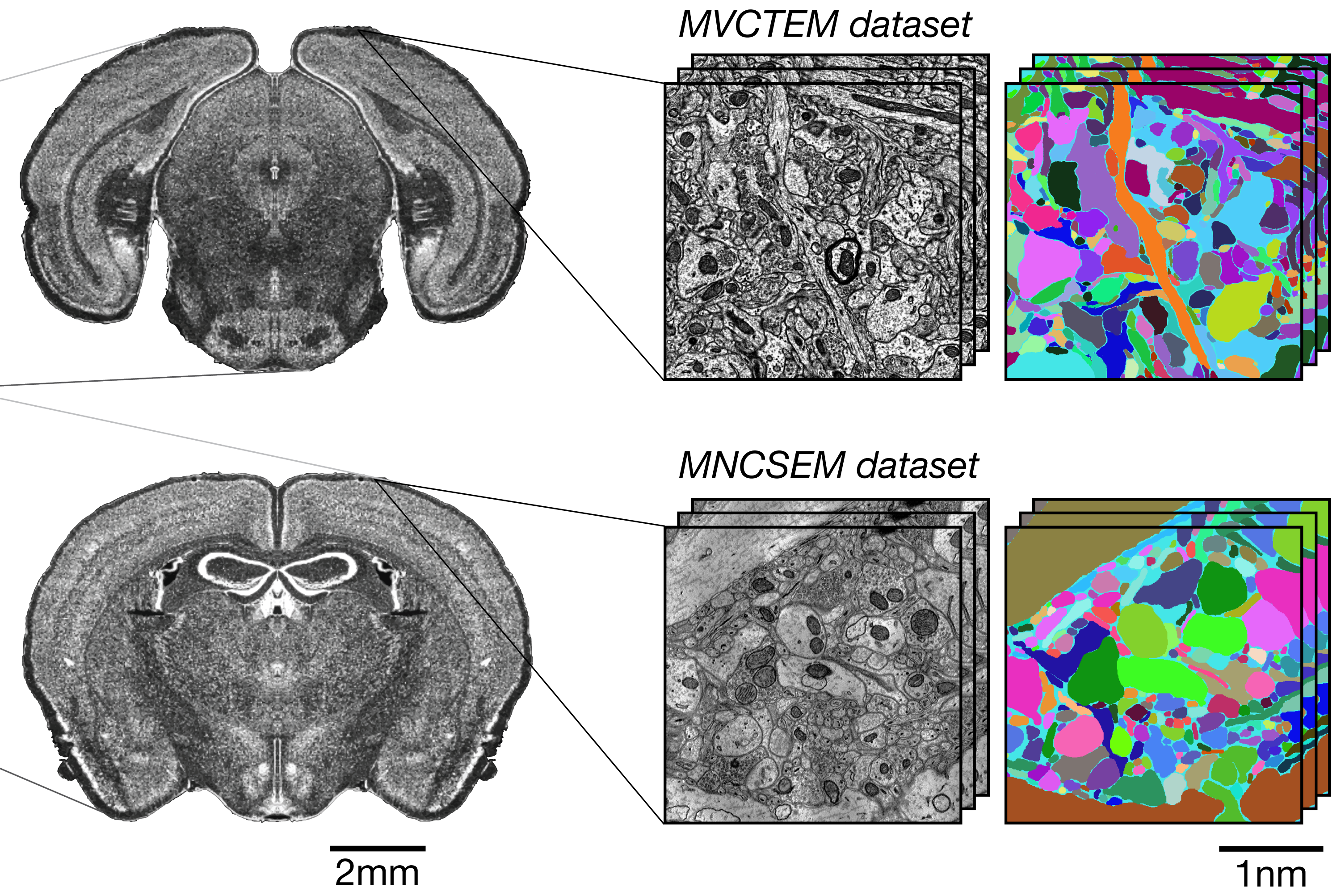
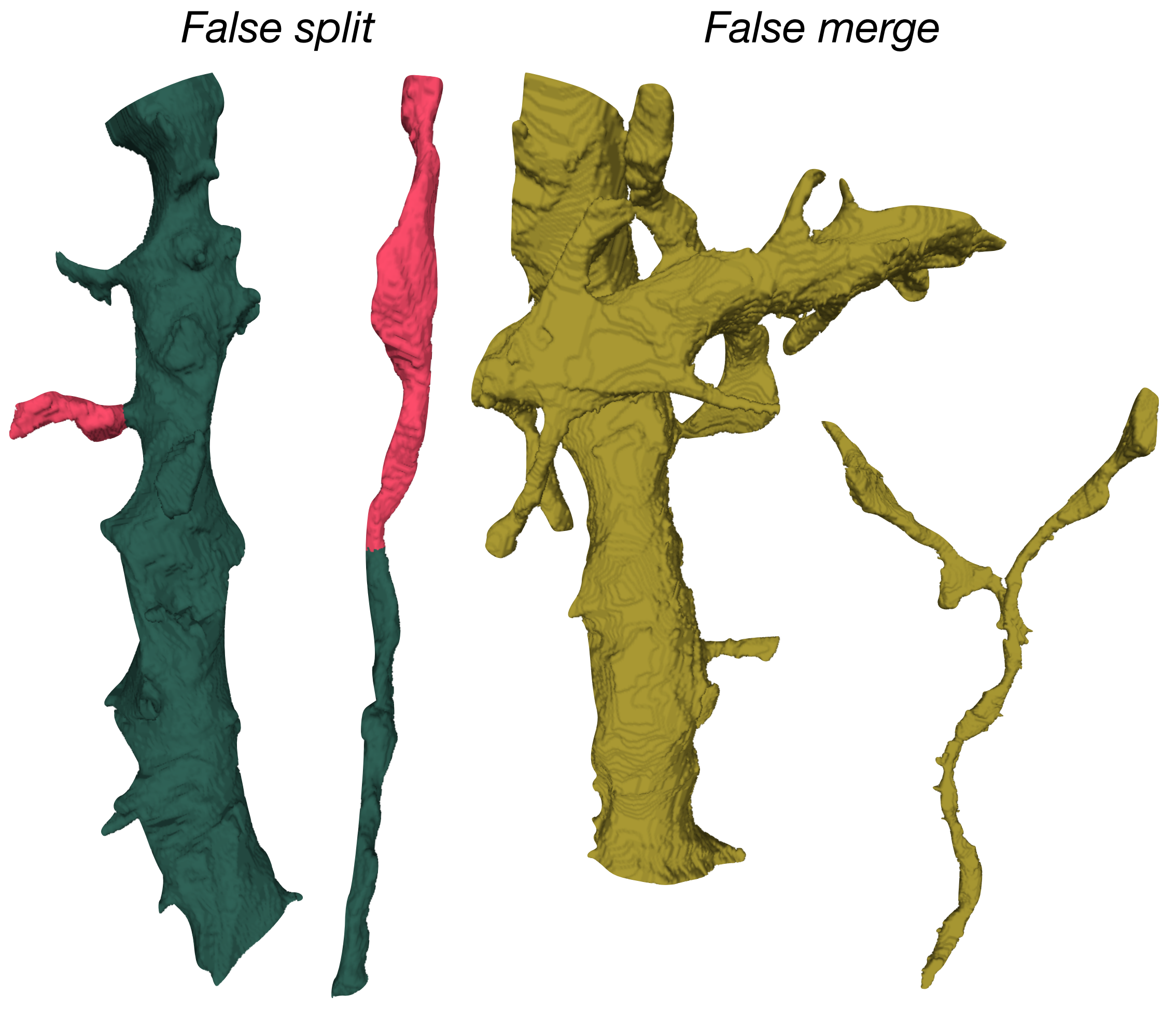
Introduction

The cellular structure of the nervous system is extremely complicated and connectomics aims to reconstruct the wiring diagram of the mammalian brain at nanometer resolution segmenting the stacks of electron microscopy (EM) images. Given the tremendous amount of data, computational solutions are required. Despite tremendous advances, current solutions still retain false merge and false-split errors. We present an efficient correction algorithm of the initial EM segmentations.



Mouse brain

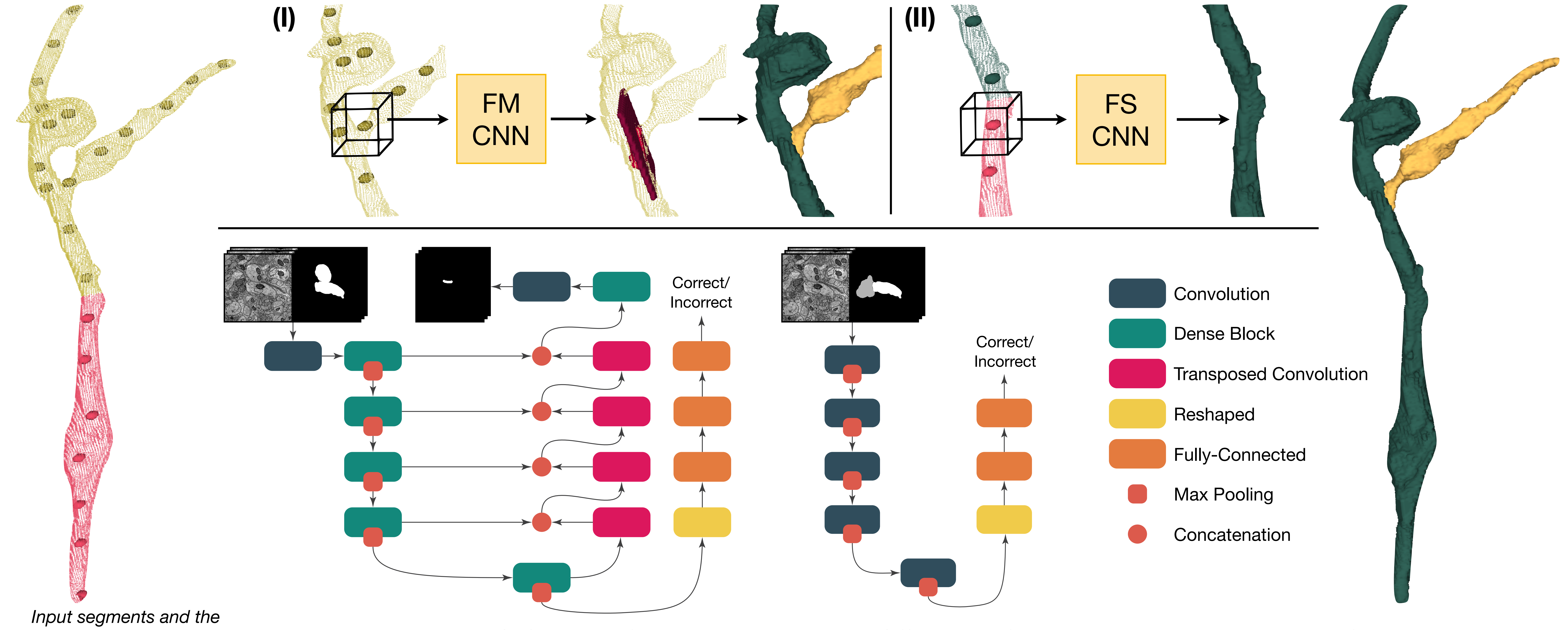




3D examples of incorrect segmentations

Method

Our algorithm consists of two successive stages: (I) false marge and (II) false split corrections. Each stage exploits a skeletal joints, generated by [1], of a segment within the input segmentation. Utilizing skeletal joints significantly reduces the number of search locations and thus enables our method to be scalable to petabyte scale reconstruction.



Input segments and the skeleton joints

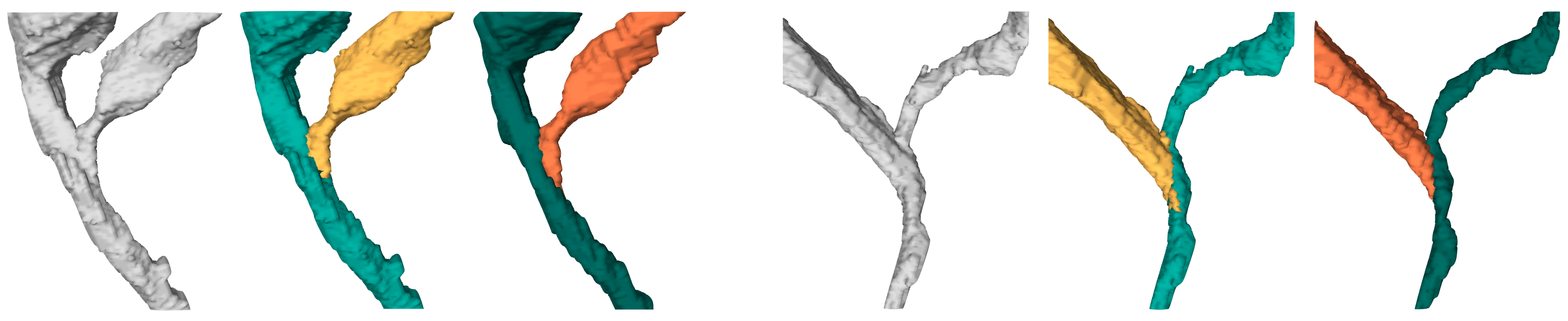
False merge (FM) correcting CNN

False split (FS) correcting CNN

Corrected segment

Results

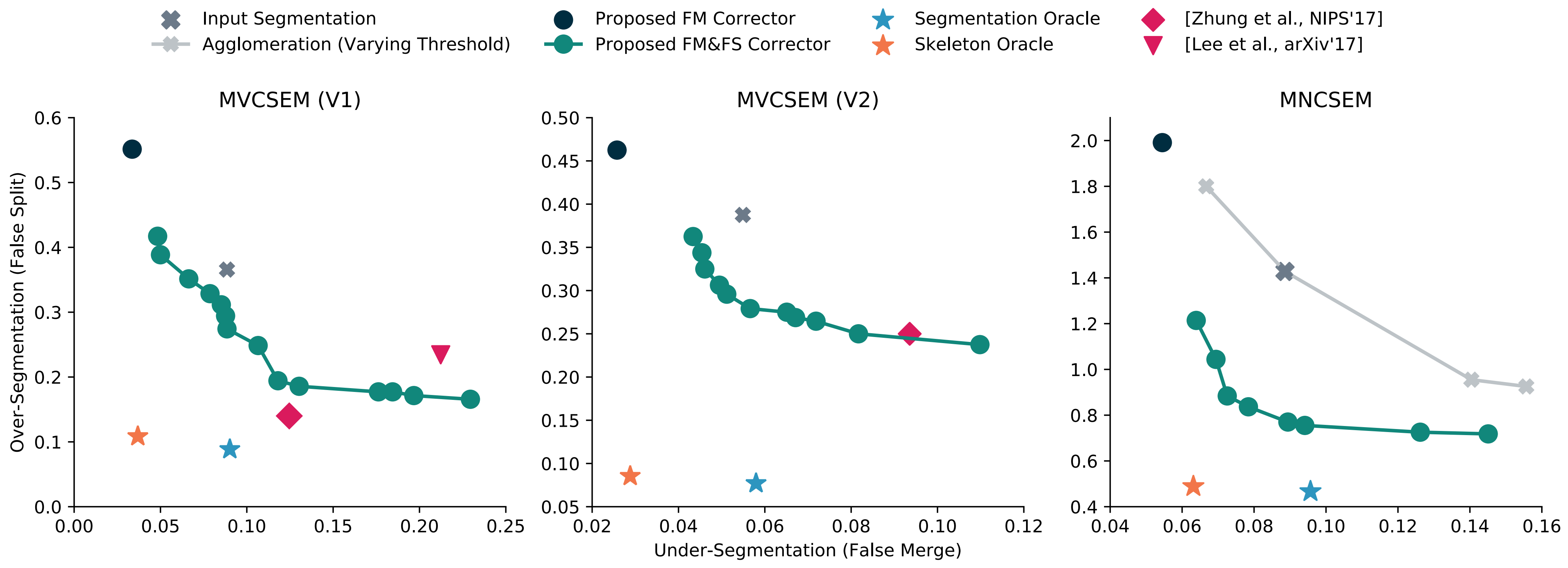
We trained and evaluated our method on the Mouse Visual Cortex TEM (MVCTEM) and Mouse Neocortex SEM (MNCSEM) datasets.



3D examples of the input, corrected and ground truth segmentations

	MVCSEM (V1)	MVCSEM (V2)	MNCTEM
Volume size (voxels)	1.07×10^9	1.07×10^9	0.816×10^9
Query points (skeleton joints)	40621	41513	62815

Search space reduction



VI curves for different experiments

Acknowledgment

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